REMARKS

Applicants enclose a paper copy and a computer readable form of a Sequence Listing. The specification has been amended to provide SEQ ID NOS for the sequences disclosed therein. The content of the paper copy and of the computer readable form is the same. This submission contains no new matter.

The Examiner is hereby invited to contact the undersigned by telephone if there are any questions concerning this amendment or application.

Respectfully submitted,

Date: March 20, 2002

Elias J. Lambiris, Reg. No. 33,728
Novozymes North America, Inc.
405 Lexington Avenue, Suite 6400
New York, NY 10174-6401
(212) 867-0123

Attorney Docket No.: 6067.200-US

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Roggen et al

Confirmation No: 2466

Serial No.: 09/733,485

Group Art Unit: 1645

Filed: December 8, 2000

Examiner: T. Bhatti

For: High Throughput Screening (HTS) Assays

VERSION WITH MARKINGS TO SHOW CHANGES MADE

Box Sequence
U.S. Patent and Trademark Office
P.O. Box 2327
Arlington, VA 22202

Sir:

Below is a marked-up version of the amendments made in the accompanying amendment.

IN THE SPECIFICATION:

The paragraph from page 41, line 15 – page 42, line 2 has been amended as follows:

In another embodiment, the library is designed, such that recognition sites for post-translational modifications are introduced in the epitope areas, and the library is expressed in a suitable host organism capable of the corresponding post-translational modification. These post-translational modifications may serve to shield the epitope and hence lower the immunogenicity of the protein variant relative to the protein backbone. Post-translational modifications include glycosylation, phosphorylation, N-terminal processing, acylation, ribosylation and sulfatation. A good example is N-glycosylation. N-glycosylation is found at sites of the sequence Asn-Xaa-Ser, Asn-Xaa-Thr, or Asn-Xaa-Cys, in which neither the Xaa residue nor the amino acid following the tri-peptide consensus sequence is a proline (T. E. Creighton, "Proteins – Structures and Molecular Properties," 2nd edition, W.H. Freeman and Co., New York, 1993, pp. 91-93). It is thus desirable to introduce such recognition sites in the sequence of the backbone protein. The specific nature of the glycosyl chain of the glycosylated protein variant may be linear or branched depending on the protein and the host cells. Another example is phosphorylation: The protein sequence can be modified so as to introduce serine phosphorylation sites with the recognition sequence arg-arg-$(xaa)_n$-ser (where n = 0, 1, or 2) (SEQ ID NOS: 1 and 2), which can be phosphorylated by the

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cAMP-dependent kinase or tyrosine phosphorylation sites with the recognition sequeence –lys/arg – $(xaa)_3$ – asp/glu – $(xaa)_3$ – tyr (SEQ ID NO: 3), which can usually be phosphorylated by tyrosine-specific kinases (T.E. Creighton, "Proteins-Structures and Molecular Properties", 2nd ed., Freeman, NY, 1993).

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